

Seminar - evolutionary macro-ecology

J. Cornuault & C. Mallon, University Groningen

Ghent University, Campus Ledeganck, 18th November 2016, 14.00-16.00

Location: lecture room 11th floor – followed by small drink

Jossilin Cornuault: Comparing the accumulation of species across multiple lineages and islands

Factors determining the accumulation of lineages on islands, through colonization and in-situ diversification are still the subject of much debate. The importance of ecological processes and geography in triggering or limiting diversification or the establishment of new colonists is still widely unknown. Discovering general trends regarding the evolutionary processes that shape diversity on islands is facilitated by macro-evolutionary studies carried out across a large taxonomic range. Comparative phylogenetic studies are particularly useful to obtain an insight into the history of multiple island lineages. However, inferring evolutionary processes from phylogenetic data for a large number of taxa and islands is impaired by multiple sources of uncertainty. These notably include uncertainty in phylogenetic data (time-calibration and topology, incomplete taxon sampling) and in inferred rates of colonization/diversification which need to be accounted for to not produce over-confident estimates of evolutionary parameters. In this context, we design a hierarchical Bayesian framework aimed for comparative phylogenetic studies that accounts for these sources of uncertainty. This basic framework can be adapted to consider varying sets of evolutionary models and/or explicative variables, facilitating the analysis of the eco-evolutionary dynamics of island taxa.

Cyrus Mallon: On the invasion of small things

Biological invasions were until recently synonymous only with macro-organisms due to the long held belief that anything smaller than one millimetre was homogenously distributed on Earth and lacked an indigenous territory. However, the advent of high-throughput DNA sequencing technology and subsequent detailed

characterization of microbes from a variety of environmental samples revealed that organisms inconspicuous to our naked eye could indeed exhibit biogeographical patterns. The fall of this conceptual barrier, paired with increasing reports of non-indigenous microbes spotted in foreign environments, has opened the door to a new perspective of life at the small-scale: microbial invasions. The use of a model system of a harmless *Escherichia coli* invading soil microbial communities has led to a better understanding of the process, patterns, and mechanisms of microbial invasions. Key among the findings is the role of biological diversity and its contribution to various resource use mechanisms, where more diverse communities better exploit available resources than less diverse communities and leave little sustenance for an invading population. Current research is focused on the cooperative interactions that may occur upon invasion, as well as understanding how biological diversity may drive the evolution of microbes and their respective communities. A mechanistic understanding of microbial invasions and community evolution has the potential to improve many practical applications where invasions and distinct community compositions of microbes are sought, like the use of bacterial biofertilizers or probiotics.